



1645

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/927,112

DATE: 01/29/2002  
TIME: 12:19:42

#5/Jan  
03-20-02

Input Set : D:\38155-20048.txt  
Output Set: N:\CRF3\01292002\I927112.raw

P.S

4 <110> APPLICANT: Millennium Pharmaceuticals, Inc.  
5 Meyers, Rachel  
6 Silos-Santiago, Inmaculada  
8 <120> TITLE OF INVENTION: 32544, a novel human phospholipase C and  
9 uses thereof  
11 <130> FILE REFERENCE: 38155-20048.00  
13 <140> CURRENT APPLICATION NUMBER: US 09/927,112  
14 <141> CURRENT FILING DATE: 2001-08-10  
16 <150> PRIOR APPLICATION NUMBER: US 60/246,808  
17 <151> PRIOR FILING DATE: 2000-11-08  
19 <160> NUMBER OF SEQ ID NOS: 17  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 4635  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Homo sapiens  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (435)...(4058)  
32 <400> SEQUENCE: 1  
33 tcgcgatcta gaactagtgg caccgctcct gcactccac tgccgcagga actgctcagg 60  
34 aacctgccgg tctccggctg ggacgggtggc tggatcagct caagcctcca gggccctgag 120  
35 gctgagggggc tgagtgtctca ttccagccgc ctccggggaac ccgggctggg agaccccatg 180  
36 cctgggggtg agcctggagc cagggcagtg cggtagagag ctccggagag agggctgggc 240  
37 accaccaggc ttgggtgtgt gatgcgtgc tggcccaggc tacacccga caagggacac 300  
38 cggggggcct gggagcagag agacctcaga gcagcctcct cctgcctcct gtggacggcc 360  
39 ggccccagct ggtgatccca gccagtccca gctttcagtt gctgccccca ccgacagtcc 420  
40 tcagtccctc catg atg gct ccc ccg aca gcc ggc ccc ctt cct ggc cca 470  
41 Met Ala Pro Pro Thr Ala Gly Pro Leu Pro Gly Pro  
42 1 5 10  
44 gct ctt ccg cct gag gac cca ggg ccg gat ccg gag agc agg tgg ctt 518  
45 Ala Leu Pro Pro Glu Asp Pro Gly Pro Asp Pro Glu Ser Arg Trp Leu  
46 15 20 25  
48 ttc ttg agc gcc aac att ctg ccc gtg gtg gag ccg tgc atg ggt gcc 566  
49 Phe Leu Ser Ala Asn Ile Leu Pro Val Val Glu Arg Cys Met Gly Ala  
50 30 35 40  
52 atg caa gag ggg atg cag atg gtg aag ctg cgt ggc ggc tcc aag ggc 614  
53 Met Gln Glu Gly Met Gln Met Val Lys Leu Arg Gly Gly Ser Lys Gly  
54 45 50 55 60  
56 ctg gtc cgc ttc tac tac ctg gac gag cac cgc tcc tgc atc cgc tgg 662  
57 Leu Val Arg Phe Tyr Tyr Leu Asp Glu His Arg Ser Cys Ile Arg Trp  
58 65 70 75  
60 agg ccc tca cgc aag aac gag aag gcc aag atc tcc atc gac tcc atc 710

ENTERED

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61	Arg	Pro	Ser	Arg	Lys	Asn	Glu	Lys	Ala	Lys	Ile	Ser	Ile	Asp	Ser	Ile	
62				80					85					90			
64	cag	gag	gtg	agt	gag	ggg	cgg	cag	tcg	gag	gtc	ttc	cag	cgc	tac	cct	758
65	Gln	Glu	Val	Ser	Glu	Gly	Arg	Gln	Ser	Glu	Val	Phe	Gln	Arg	Tyr	Pro	
66			95				100					105					
68	gac	ggc	agc	ttc	gac	ccc	aac	tgc	tgc	ttc	agc	atc	tac	cac	ggc	agc	806
69	Asp	Gly	Ser	Phe	Asp	Pro	Asn	Cys	Cys	Phe	Ser	Ile	Tyr	His	Gly	Ser	
70		110					115					120					
72	cac	cgc	gag	tcg	ctg	gac	ctg	gtc	tcc	acc	agc	agc	gag	gtg	gcg	cgc	854
73	His	Arg	Glu	Ser	Leu	Asp	Leu	Val	Ser	Thr	Ser	Ser	Glu	Val	Ala	Arg	
74	125					130						135				140	
76	acc	tgg	gtc	act	ggc	ctg	cgc	tac	ctc	atg	gcc	ggc	atc	agc	gac	gag	902
77	Thr	Trp	Val	Thr	Gly	Leu	Arg	Tyr	Leu	Met	Ala	Gly	Ile	Ser	Asp	Glu	
78				145						150					155		
80	gac	agc	ctg	gct	cgc	cgc	cag	cgc	acc	agg	gac	cag	tgg	ctg	aag	cag	950
81	Asp	Ser	Leu	Ala	Arg	Arg	Gln	Arg	Thr	Arg	Asp	Gln	Trp	Leu	Lys	Gln	
82			160						165			170					
84	acg	ttt	gac	gag	gcc	gac	aag	aac	ggg	gat	ggc	agc	ctg	agc	att	ggc	998
85	Thr	Phe	Asp	Glu	Ala	Asp	Lys	Asn	Gly	Asp	Gly	Ser	Leu	Ser	Ile	Gly	
86		175					180					185					
88	gag	gtc	ctg	cag	ctg	ctg	cac	aag	ctc	aac	gtg	aac	ctg	ccc	cgg	cag	1046
89	Glu	Val	Leu	Gln	Leu	Leu	His	Lys	Leu	Asn	Val	Asn	Leu	Pro	Arg	Gln	
90		190					195					200					
92	agg	gtg	aag	cag	atg	ttc	agg	gaa	gcg	gac	acg	gat	gac	cac	caa	ggg	1094
93	Arg	Val	Lys	Gln	Met	Phe	Arg	Glu	Ala	Asp	Thr	Asp	Asp	His	Gln	Gly	
94	205					210					215				220		
96	acg	ctg	ggt	ttt	gaa	gag	ttc	tgt	gcc	ttc	tac	aag	atg	atg	tcc	acc	1142
97	Thr	Leu	Gly	Phe	Glu	Glu	Phe	Cys	Ala	Phe	Tyr	Lys	Met	Met	Ser	Thr	
98			225						230				235				
100	cgc	cgg	gac	ctc	tac	ctg	ctc	atg	ctg	acc	tac	agc	aac	cac	aag	gac	1190
101	Arg	Arg	Asp	Leu	Tyr	Leu	Leu	Met	Leu	Thr	Tyr	Ser	Asn	His	Lys	Asp	
102			240						245				250				
104	cac	ctg	gat	gcc	gcc	agc	ctg	cag	cgc	ttc	ctg	cag	gtg	gag	cag	aag	1238
105	His	Leu	Asp	Ala	Ala	Ser	Leu	Gln	Arg	Phe	Leu	Gln	Val	Glu	Gln	Lys	
106		255					260					265					
108	atg	gcg	ggt	gtg	acc	ctc	gag	agc	tgc	cag	gac	atc	atc	gag	cag	ttt	1286
109	Met	Ala	Gly	Val	Thr	Leu	Glu	Ser	Cys	Gln	Asp	Ile	Ile	Glu	Gln	Phe	
110		270					275					280					
112	gag	cca	tgc	cca	gaa	aac	aag	agt	aag	ggg	ctg	ctg	ggc	att	gat	ggc	1334
113	Glu	Pro	Cys	Pro	Glu	Asn	Lys	Ser	Lys	Gly	Leu	Leu	Gly	Ile	Asp	Gly	
114	285					290					295				300		
116	ttc	acc	aac	tac	acc	agg	agc	cct	gct	ggt	gac	atc	ttc	aac	cct	gag	1382
117	Phe	Thr	Asn	Tyr	Thr	Arg	Ser	Pro	Ala	Gly	Asp	Ile	Phe	Asn	Pro	Glu	
118			305						310				315				
120	cac	cac	cat	gtg	cac	cag	gac	atg	acg	cag	ccg	ctg	agc	cac	tac	ttc	1430
121	His	His	His	Val	His	Gln	Asp	Met	Thr	Gln	Pro	Leu	Ser	His	Tyr	Phe	
122			320						325				330				
124	atc	acc	tcg	tcc	cac	aac	acc	tac	ctc	gtg	ggt	gac	cag	ctc	atg	tcc	1478
125	Ile	Thr	Ser	Ser	His	Asn	Thr	Tyr	Leu	Val	Gly	Asp	Gln	Leu	Met	Ser	

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126	335	340	345	
128	cag tca cgg gtg gac atg tat gct tgg gtc ctg cag gct ggc tgc cgc	1526		
129	Gln Ser Arg Val Asp Met Tyr Ala Trp Val Leu Gln Ala Gly Cys Arg			
130	350	355	360	
132	tgc gtg gag gtg gac tgc tgg gat ggg ccc gac ggg gag ccc att gtg	1574		
133	Cys Val Glu Val Asp Cys Trp Asp Gly Pro Asp Gly Glu Pro Ile Val			
134	365	370	375	380
136	cac cat ggc tac act ctg act tcc aag atc ctc ttc aaa gac gtc att	1622		
137	His His Gly Tyr Thr Leu Thr Ser Lys Ile Leu Phe Lys Asp Val Ile			
138	385	390	395	
140	gaa acc atc aac aaa tat gcc ttc atc aag aat gag tac cca gtg atc	1670		
141	Glu Thr Ile Asn Lys Tyr Ala Phe Ile Lys Asn Glu Tyr Pro Val Ile			
142	400	405	410	
144	ctg tcc atc gaa aac cac tgc agt gtc atc cag cag aag aaa atg gcc	1718		
145	Leu Ser Ile Glu Asn His Cys Ser Val Ile Gln Gln Lys Lys Met Ala			
146	415	420	425	
148	cag tat ctg act gac atc ctt ggg gac aag ctg gac ctg tca tca gtg	1766		
149	Gln Tyr Leu Thr Asp Ile Leu Gly Asp Lys Leu Asp Leu Ser Ser Val			
150	430	435	440	
152	agc agt gaa gat gcc acc aca ctc ccc tct cca cag atg ctc aag ggc	1814		
153	Ser Ser Glu Asp Ala Thr Thr Leu Pro Ser Pro Gln Met Leu Lys Gly			
154	445	450	455	460
156	aag atc ctc gtg aag ggg aag aag ctc cca gcc aac atc agc gag gat	1862		
157	Lys Ile Leu Val Lys Gly Lys Lys Leu Pro Ala Asn Ile Ser Glu Asp			
158	465	470	475	
160	gcg gag gaa ggc gag gtg tct gat gag gac agt gct gat gag att gac	1910		
161	Ala Glu Glu Gly Glu Val Ser Asp Glu Asp Ser Ala Asp Glu Ile Asp			
162	480	485	490	
164	gat gac tgc aag ctc ctc aat ggg gat gca tcc acc aat cga aag cgt	1958		
165	Asp Asp Cys Lys Leu Leu Asn Gly Asp Ala Ser Thr Asn Arg Lys Arg			
166	495	500	505	
168	gta gaa aac act gct aag agg aaa ctg gat tcc ctc atc aaa gag tcg	2006		
169	Val Glu Asn Thr Ala Lys Arg Lys Leu Asp Ser Leu Ile Lys Glu Ser			
170	510	515	520	
172	aag att cgg gac tgt gag gac ccc aac aac ttc tcc gtc tcc aca ctg	2054		
173	Lys Ile Arg Asp Cys Glu Asp Pro Asn Asn Phe Ser Val Ser Thr Leu			
174	525	530	535	540
176	tcc cca tct gga aag ctc gga cgc aag agc aag gct gaa gag gac gtg	2102		
177	Ser Pro Ser Gly Lys Leu Gly Arg Lys Ser Lys Ala Glu Glu Asp Val			
178	545	550	555	
180	gag tct ggg gag gat gcc ggg gcc agc aga cgc aat ggc cgc ctc gtc	2150		
181	Glu Ser Gly Glu Asp Ala Gly Ala Ser Arg Arg Asn Gly Arg Leu Val			
182	560	565	570	
184	gtg gga agc ttc tcc agg cgc aag aag aag ggc agc aag ctg aag aag	2198		
185	Val Gly Ser Phe Ser Arg Arg Lys Lys Lys Gly Ser Lys Leu Lys Lys			
186	575	580	585	
188	gcg gcc agc gtg gag gag gga gat gag ggt cag gac tcc ccg gga ggc	2246		
189	Ala Ala Ser Val Glu Glu Gly Asp Glu Gly Gln Asp Ser Pro Gly Gly			
190	590	595	600	

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192	cag	agc	cga	ggg	gcg	acc	cgg	cag	aag	aag	acc	atg	aag	ctg	tcc	cgg	2294
193	Gln	Ser	Arg	Gly	Ala	Thr	Arg	Gln	Lys	Lys	Thr	Met	Lys	Leu	Ser	Arg	
194	605					610					615					620	
196	gcc	ctc	tct	gac	ctg	gtg	aag	tac	acc	aag	tcc	gtg	gcc	acc	cac	gac	2342
197	Ala	Leu	Ser	Asp	Leu	Val	Lys	Tyr	Thr	Lys	Ser	Val	Ala	Thr	His	Asp	
198					625					630					635		
200	ata	gag	atg	gag	gcg	gcg	tcc	agc	tgg	cag	gtg	tcg	tcc	ttc	agc	gag	2390
201	Ile	Glu	Met	Glu	Ala	Ala	Ser	Ser	Trp	Gln	Val	Ser	Ser	Phe	Ser	Glu	
202				640					645					650			
204	acc	aag	gcc	cac	cag	att	ctg	cag	cag	aag	ccg	gcg	cag	tac	cta	cgc	2438
205	Thr	Lys	Ala	His	Gln	Ile	Leu	Gln	Lys	Pro	Ala	Gln	Tyr	Leu	Arg		
206			655				660				665						
208	ttc	aac	cag	cag	ctc	tcc	cgc	atc	tac	ccc	tcc	tcc	tac	cgt	gtg		2486
209	Phe	Asn	Gln	Gln	Gln	Leu	Ser	Arg	Ile	Tyr	Pro	Ser	Ser	Tyr	Arg	Val	
210		670				675					680						
212	gac	tcc	agc	aac	tac	aac	ccg	cag	ccc	ttc	tgg	aac	gcc	ggc	tgc	caa	2534
213	Asp	Ser	Ser	Asn	Tyr	Asn	Pro	Gln	Pro	Phe	Trp	Asn	Ala	Gly	Cys	Gln	
214	685					690				695						700	
216	atg	gtt	gcc	ctg	aac	tac	cag	tca	gag	ggg	cgg	atg	ctg	cag	ctg	aac	2582
217	Met	Val	Ala	Leu	Asn	Tyr	Gln	Ser	Glu	Gly	Arg	Met	Leu	Gln	Leu	Asn	
218				705					710					715			
220	cga	gcc	aag	ttc	agc	gcc	aac	ggt	ggc	tgc	ggc	tac	gta	ctc	aag	cct	2630
221	Arg	Ala	Lys	Phe	Ser	Ala	Asn	Gly	Gly	Cys	Gly	Tyr	Val	Leu	Lys	Pro	
222			720					725					730				
224	ggg	tgc	atg	tgc	cag	ggc	gtg	ttc	aac	ccc	aac	tcg	gag	gac	ccc	ctg	2678
225	Gly	Cys	Met	Cys	Gln	Gly	Val	Phe	Asn	Pro	Asn	Ser	Glu	Asp	Pro	Leu	
226			735				740				745						
228	ccc	ggg	cag	ctc	aag	aag	cag	ctg	gtg	ctc	cgg	atc	atc	agt	ggc	cag	2726
229	Pro	Gly	Gln	Leu	Lys	Lys	Gln	Leu	Val	Leu	Arg	Ile	Ile	Ser	Gly	Gln	
230		750				755					760						
232	cag	ctt	ccc	aag	ccg	cgc	gac	tcc	atg	ctg	ggg	gac	cgt	ggg	gag	atc	2774
233	Gln	Leu	Pro	Lys	Pro	Arg	Asp	Ser	Met	Leu	Gly	Asp	Arg	Gly	Glu	Ile	
234	765				770				775					780			
236	atc	gac	ccc	ttt	gtg	gag	gtg	gag	atc	att	ggg	ctc	cct	gtg	gac	tgc	2822
237	Ile	Asp	Pro	Phe	Val	Glu	Val	Glu	Ile	Ile	Gly	Leu	Pro	Val	Asp	Cys	
238				785					790					795			
240	agc	agg	gag	cag	acc	cgc	gtg	gtg	gac	gac	aac	ggg	ttc	aac	ccc	acc	2870
241	Ser	Arg	Glu	Gln	Thr	Arg	Val	Val	Asp	Asp	Asn	Gly	Phe	Asn	Pro	Thr	
242			800					805					810				
244	tgg	gag	gag	acc	ctg	gtt	ttc	atg	gtg	cac	atg	ccg	gag	atc	gcg	ctg	2918
245	Trp	Glu	Glu	Thr	Leu	Val	Phe	Met	Val	His	Met	Pro	Glu	Ile	Ala	Leu	
246		815				820						825					
248	gtc	cgc	ttc	ctc	gtc	tgg	gac	cac	gat	ccc	atc	ggg	cgt	gac	ttc	att	2966
249	Val	Arg	Phe	Leu	Val	Trp	Asp	His	Asp	Pro	Ile	Gly	Arg	Asp	Phe	Ile	
250		830				835					840						
252	ggc	cag	agg	acg	ctg	gcc	ttc	agc	agc	atg	atg	cca	ggc	tac	aga	cac	3014
253	Gly	Gln	Arg	Thr	Leu	Ala	Phe	Ser	Ser	Met	Met	Pro	Gly	Tyr	Arg	His	
254	845				850				855					860			
256	gtg	tac	cta	gaa	ggg	atg	gaa	gag	gcc	tcc	atc	ttc	gtg	cat	gtg	gct	3062

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257 Val Tyr Leu Glu Gly Met Glu Glu Ala Ser Ile Phe Val His Val Ala
258                      865                      870                      875
260 gtc agt gac atc agc ggt aag gtc aag cag gct ctg ggc cta aaa ggc      3110
261 Val Ser Asp Ile Ser Gly Lys Val Lys Gln Ala Leu Gly Leu Lys Gly
262                      880                      885                      890
264 ctc ttc ctc cga ggc cca aag ccc ggc tcg ctg gac agt cat gct gct      3158
265 Leu Phe Leu Arg Gly Pro Lys Pro Gly Ser Leu Asp Ser His Ala Ala
266                      895                      900                      905
268 ggg cgg ccc ccg gcc cgg ccc tcc gtt agc cag cgg atc ctg cgg cgc      3206
269 Gly Arg Pro Pro Ala Arg Pro Ser Val Ser Gln Arg Ile Leu Arg Arg
270                      910                      915                      920
272 acg gcc agc gcc ccg acc aag agc cag aag ccg ggc cgc agg ggc ttc      3254
273 Thr Ala Ser Ala Pro Thr Lys Ser Gln Lys Pro Gly Arg Arg Gly Phe
274 925                      930                      935                      940
276 ccg gag ctg gtc ctg ggt aca cgg gac aca ggc tcc aag ggg gtg gca      3302
277 Pro Glu Leu Val Leu Gly Thr Arg Asp Thr Gly Ser Lys Gly Val Ala
278                      945                      950                      955
280 gac gat gtg gtg ccc ccc ggg ccc gga cct gct ccg gaa gcc cca gcc      3350
281 Asp Asp Val Val Pro Pro Gly Pro Gly Pro Ala Pro Glu Ala Pro Ala
282                      960                      965                      970
284 cag gag ggg ccc ggc agc ggc agc ccc cga ggt aag gcg cca gct gcg      3398
285 Gln Glu Gly Pro Gly Ser Gly Ser Pro Arg Gly Lys Ala Pro Ala Ala
286                      975                      980                      985
288 gtg gca gag aag agc cct gtg cga gtg cgg ccc ccg cgt gtc ctg gac      3446
289 Val Ala Glu Lys Ser Pro Val Arg Val Arg Pro Pro Arg Val Leu Asp
290                      990                      995                      1000
292 ggc ccc ggg cct gct ggg atg gcc gcc aca tgc atg aag tgt gtg gtg      3494
293 Gly Pro Gly Pro Ala Gly Met Ala Ala Thr Cys Met Lys Cys Val Val
294 1005                      1010                      1015                      1020
296 gga tcc tgc gcc ggc gtg aac acc ggg ggc ctg cag agg gag cgg cca      3542
297 Gly Ser Cys Ala Gly Val Asn Thr Gly Gly Leu Gln Arg Glu Arg Pro
298                      1025                      1030                      1035
300 ccc agc ccg ggg cct gca agc agg cag gca gcc att cgc cag cag ccc      3590
301 Pro Ser Pro Gly Pro Ala Ser Arg Gln Ala Ala Ile Arg Gln Gln Pro
302                      1040                      1045                      1050
304 cgg gcc cgg gct gac tca ctg ggg gcc ccc tgc tgt ggc ctg gac cct      3638
305 Arg Ala Arg Ala Asp Ser Leu Gly Ala Pro Cys Cys Gly Leu Asp Pro
306                      1055                      1060                      1065
308 cac gct atc ccg ggg aga agc aga gag gcc ccc aag ggt cct ggg gcc      3686
309 His Ala Ile Pro Gly Arg Ser Arg Glu Ala Pro Lys Gly Pro Gly Ala
310                      1070                      1075                      1080
312 tgg agg cag ggt cca ggc ggt agc ggc tcc atg tcc tcg gac tcc agc      3734
313 Trp Arg Gln Gly Pro Gly Gly Ser Gly Ser Met Ser Ser Asp Ser Ser
314 1085                      1090                      1095                      1100
316 agc cca gac agc ccg ggc atc ccc gaa agg tcc ccc cgc tgg cct gag      3782
317 Ser Pro Asp Ser Pro Gly Ile Pro Glu Arg Ser Pro Arg Trp Pro Glu
318                      1105                      1110                      1115
320 ggt gcc tgc agg caa ccg ggg gcc ctg cag gga gag atg agt gcc ttg      3830
321 Gly Ala Cys Arg Gln Pro Gly Ala Leu Gln Gly Glu Met Ser Ala Leu

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/927,112

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L:919 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:923 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17